

P:\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 1 -

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

<120> NOVEL GENETIC SEQUENCES ENCODING STEROID AND JUVENILE HORMONE

5 RECEPTOR POLYPEPTIDES AND INSECTICIDAL MODALITIES THEREFOR II

<130> p:\oper\mro\ecdysone.cip

<140> US continuation-in-part of PCT/AU99/00033

<141> 1999-07-02

10 <150> PCT/AU/00033

<151> 1999-01-15

<150> AU PP1536

<151> 1998-01-15

15

<160> 20

<170> PatentIn Ver. 2.0

<210> 1

20 <211> 2274

<212> DNA

<213> Lucilia cuprina

<220>

25 <221> CDS

<222> (1) . . (2271)

<400> 1

atg atg aaa cga cgt tgg tct aat aat ggc ggt ttt gcc gct tta aaa 48

30 Met Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Ala Ala Leu Lys

1

5

10

15

P:\OPER\MRO\EC DYSONE.CIP - 1/7/99

- 4 -

agt ctt aat ggc ttc tca aca agc gat gct agt gat gtt aag aaa atc 864
 Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile
 275 280 285

5 aaa aaa ggt cct gcg ccc cgt tta caa gag gaa ctg tgt ctg gtg tgt 912
 Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys
 290 295 300

ggg gat cgg gcg tcc ggt tat cat tat aac gca ctc acc tgt gaa ggc 960
 10 Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly
 305 310 315 320

tgt aag ggg ttc ttt cga cgg agt gtt acc aaa aat gcg gtg tat tgt 1008
 Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Cys
 15 325 330 335

tgt aaa ttt ggt cat gcc tgc gaa atg gac atg tat atg cga cgt aaa 1056
 Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys
 340 345 350

20 tgt cag gaa tgt agg ctg aaa.aaa tgt ttg gct gtg ggc atg cgg ccg 1104
 Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro
 355 360 365

25 gaa tgt gtg gtg ccc gaa aac cag tgt gca atg aaa cga cgc gaa aag 1152
 Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys
 370 375 380

667020"049460

P:\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 6 -

gag gat caa ata aca cta tta aag gcc tgc tca tca gaa gtt atg atg 1584

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met

515

520

525

5 ttg cga atg gca cga cgt tac gat cac aat tca gat tgg ata ttc ttt 1632

Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe

530

535

540

cc aat aat cga tcg tat acg cgt gac tct tat aaa atg gct ggc atg 1680

10 Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met

545

550

555

560

gct gat aat att gag gat ctg ctg cat ttc tgt cga caa atg tac tcg 1728

Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ser

15

565

570

575

atg aaa gtg gac aat gtc gaa tat gct cta ctc aet gcc att gtg atc 1776

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile

580

585

590

20

ttt tcc gat cgg ccg ggc ctc gaa gaa ggc gaa cta gtc gaa gccg ata 1824

Phe Ser Asp Arg Pro Gly Leu Glu Glu Ala Glu Leu Val Glu Ala Ile

595

600

605

25 caa agt tac tac atc gat aca ctc cgc att tac ata ctt aat cgc cat 1872

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His

610

615

620

tgc ggc gat ccc atg agt ctc gta ttc ttt gcc aag ctt ctg tca att 1920

30 Cys Gly Asp Pro Met Ser Leu Val Phe Phe Ala Lys Leu Leu Ser Ile

625

630

635

640

- 7 -

caa tcg gat aat gca tag 2274

30 Gln Ser Asp Asn Ala

755

- 9 -

140

160

175

190

205

220

240

255

270

285

Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys

- 10 -

300

5

10

15

20

25

30

Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
450 455 460

P:\OPER\IMRO\ECODYSONE.CIP - 1/7/99

- 11 -

Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp

465 470 475 480

Ala Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu

5 485 490 495

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln

500 505 510

10

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met

515 520 525

Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe

15 530 535 540

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met

545 550 555 560

20 Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ser

565 570 575

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile

580 585 590

25

Phe Ser Asp Arg Pro Gly Leu Glu Glu Ala Glu Leu Val Glu Ala Ile

595 600 605

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His

30 610 615 620

607040 "0431600

P:\OPER\MRO\ECDYSONE.CIP - 1/7/9

[illegible]

<213> Lucillia cuprina

P:OPER\MRO\ECDYSONE,CIP-17

- 13 -

<220>

<221> CDS

<222> (1)..(1401)

5

<400> 1

atg gat aac ggc gag caa gat gct ggg ttc cga ttg gca ccg atg tct 48
 Met Asp Asn Gly Glu Gln Asp Ala Gly Phe Arg Leu Ala Pro Met Ser
 1 5 10 15

ccg cag gag ata aag cca gac att tca cta ctc aat gaa aat aat acg 96
 Pro Gln Glu Ile Lys Pro Asp Ile Ser Leu Leu Asn Glu Asn Asn Thr
 20 25 30

agt agt tat tcg ccc aaa cct gga agt cct aat cca ttt gcc atc gga 144
 Ser Ser Tyr Ser Pro Lys Pro Gly Ser Pro Asn Pro Phe Ala Ile Gly
 35 40 45

ttg cag gca ata aat gca gtc gct gcc gcg aat gcc aat aac caa aat 192
 Leu Gln Ala Ile Asn Ala Val Ala Ala Ala Asn Ala Asn Asn Gln Asn
 50 55 60

caa atg ttg caa act acg cca cca caa cag cag cag tat cca cca aat 240
 Gln Met Leu Gln Thr Thr Pro Pro Gln Gln Gln Gln Tyr Pro Pro Asn
 65 70 75 80

cac ccc ctt agt ggt tcg aaa cac ttg tgt tcc att tgt gga gac cgc 288
 His Pro Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg
 85 90 95

gcc agt gga aaa cat tat ggg gtc tac agt tgt gag ggt tgt aaa ggg 336
 Ala Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly
 100 105 110

ttc ttc aaa cgt acc gta cgc aag gac ttg aca tat gct tgt cgt gag 384
 Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu
 115 120 125

gac aga aat tgc att ata gat aaa cga caa aga aat cgt tgc cag tat 432
 Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr
 130 135 140

tgt cgt tat caa aag tgt tta gct tgt ggc atg aaa cgc gaa gcg gtc 480
 Cys Arg Tyr Gln Lys Cys Leu Ala Cys Gly Met Lys Arg Glu Ala Val

66702002437660

P:\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 14 -

	145	150	155	160	
5	caa gag gaa cga caa cgt ggt act cgt gct gct aac gct aga gct gct				528
	Gln Glu Glu Arg Gln Arg Gly Thr Arg Ala Ala Asn Ala Arg Ala Ala				
10		165	170	175	
15	ggt gct ggc ggt ggt gga gga ggt ggt ggt ggt gta agc aat gtg gtt				576
	Gly Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Val Ser Asn Val Val				
		180	185	190	
20	ggt gct ggc gga gaa gac ttt aaa ccc agc agt tca tta cgt gat ctc				624
	Gly Ala Gly Gly Glu Asp Phe Lys Pro Ser Ser Ser Leu Arg Asp Leu				
25		195	200	205	
30	act ata gaa cgc atc att gaa gcc gag caa aag gct gaa tct ttg agc				672
	Thr Ile Glu Arg Ile Ile Glu Ala Glu Gln Lys Ala Glu Ser Leu Ser				
		210	215	220	
35	ggt gat aac gtg ttg ccc ttt ttg cgc gtt ggc aac aat tcc atg gta				720
	Gly Asp Asn Val Leu Pro Phe Leu Arg Val Gly Asn Asn Ser Met Val				
40		225	230	235	240
45	caa cac gac tac aaa ggc gcg gta tct cat ctc tgc cag atg gtt aac				768
	Gln His Asp Tyr Lys Gly Ala Val Ser His Leu Cys Gln Met Val Asn				
50		245	250	255	
55	aaa caa ctc tac caa atg gtt gaa tat gca cgt cga aca cca cat ctt				816
	Lys Gln Leu Tyr Gln Met Val Glu Tyr Ala Arg Arg Thr Pro His Phe				
		260	265	270	
60	aca cat ttg cag cgt gag gat cag ata cta ttg tta aag gct ggc tgg				864
	Thr His Leu Gln Arg Glu Asp Gln Ile Leu Leu Leu Lys Ala Gly Trp				
65		275	280	285	
70	aat gaa ctg cta att gca aat gtt gcc tgg tgc agt att gag tct ctg				912
	Asn Glu Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Glu Ser Leu				
		290	295	300	
75	gat gcc gaa tat gcc tct cct ggt acg gta cat gac ggt tct ttt ggt				960
	Asp Ala Glu Tyr Ala Ser Pro Gly Thr Val His Asp Gly Ser Phe Gly				
80		305	310	315	320
85	egg cgt tca cca gtg cgt cag ccc caa caa ctc ttc ctt aat cag aat				1008
	Arg Arg Ser Pro Val Arg Gln Pro Gln Gln Leu Phe Leu Asn Gln Asn				
90		325	330	335	

PROPERIMROECDYSONE.CIP - 177

- 15 -

	ttc tcg tat cat cgc aat agt gct att aag gcc aat gtt gtt tca att	1056
5	Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Asn Val Val Ser Ile 340 345 350	
10	ttc gat cgt atc ctc tcg gag ttg agc atc aaa atg aaa cgt ctt aac	1104
	Phe Asp Arg Ile Leu Ser Glu Leu Ser Ile Lys Met Lys Arg Leu Asn 355 360 365	
15	atc gat cgc tcg gag ttg tcg tgt ctg aag gca atc ata ctc ttc aat	1152
20	Ile Asp Arg Ser Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Phe Asn 370 375 380	
25	cca gac ata cgc ggt ctg aaa tgt cga gcc gac gtc gag gta tgt cgt	1200
30	Pro Asp Ile Arg Gly Leu Lys Cys Arg Ala Asp Val Glu Val Cys Arg 385 390 395 400	
35	gaa aaa atc tat gcc tgt ctg gac gaa cac tgc cgc aca gaa cat cca	1248
	Glu Lys Ile Tyr Ala Cys Leu Asp Glu His Cys Arg Thr Glu His Pro 405 410 415	
40	ggc gat gat ggc cgc ttt gct cag cta cta cta agg ttg ccc gca ttg	1296
45	Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Pro Ala Leu 420 425 430	
50	cgt tcc atc agt ctc aaa tgt ctc gat cat ttg ttt ttc ttc cgt tta	1344
	Arg Ser Ile Ser Leu Lys Cys Leu Asp His Leu Phe Phe Phe Arg Leu 435 440 445	
55	ata ggc gaa aga gca ttg gag gaa tta att gct gag caa ttg gaa gct	1392
60	Ile Gly Glu Arg Ala Leu Glu Glu Leu Ile Ala Glu Gln Leu Glu Ala 450 455 460	
65	cct atc tgc	1401
	Pro Ile Cys	
70	465	
75	<210> 4	
	<211> 467	
80	<212> PRT	
	<213> Lucillia cuprina	
85	<400> 4	
	Met Asp Asn Gly Glu Gln Asp Ala Gly Phe Arg Leu Ala Pro Met Ser	
90	1 5 10 15	

PI\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 16 -

	Pro	Gln	Glu	Ile	Lys	Pro	Asp	Ile	Ser	Leu	Leu	Asn	Glu	Asn	Asn	Thr	
					20					25						30	
5																	
	Ser	Ser	Tyr	Ser	Pro	Lys	Pro	Gly	Ser	Pro	Asn	Pro	Phe	Ala	Ile	Gly	
10				35				40						45			
	Leu	Gln	Ala	Ile	Asn	Ala	Val	Ala	Ala	Ala	Asn	Ala	Asn	Asn	Gln	Asn	
15			50				55					60					
	Gln	Met	Leu	Gln	Thr	Thr	Pro	Pro	Gln	Gln	Gln	Gln	Tyr	Pro	Pro	Asn	
20		65				70					75					80	
	His	Pro	Leu	Ser	Gly	Ser	Lys	His	Leu	Cys	Ser	Ile	Cys	Gly	Asp	Arg	
25					85					90						95	
30																	
	Ala	Ser	Gly	Lys	His	Tyr	Gly	Val	Tyr	Ser	Cys	Glu	Gly	Cys	Lys	Gly	
35				100					105						110		
	Phe	Phe	Lys	Arg	Thr	Val	Arg	Lys	Asp	Leu	Thr	Tyr	Ala	Cys	Arg	Glu	
40			115					120					125				
	Asp	Arg	Asn	Cys	Ile	Ile	Asp	Lys	Arg	Gln	Arg	Asn	Arg	Cys	Gln	Tyr	
45		130					135					140					
	Cys	Arg	Tyr	Gln	Lys	Cys	Leu	Ala	Cys	Gly	Met	Lys	Arg	Glu	Ala	Val	
50		145				150					155					160	
	Gln	Glu	Glu	Arg	Gln	Arg	Gly	Thr	Arg	Ala	Ala	Asn	Ala	Arg	Ala	Ala	
55					165					170						175	
60																	
	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Val	Ser	Asn	Val	Val	
65				180						185					190		
	Gly	Ala	Gly	Gly	Glu	Asp	Phe	Lys	Pro	Ser	Ser	Ser	Leu	Arg	Asp	Leu	
70			195					200					205				
	Thr	Ile	Glu	Arg	Ile	Ile	Glu	Ala	Glu	Gln	Lys	Ala	Glu	Ser	Leu	Ser	
75			210				215					220					
	Gly	Asp	Asn	Val	Leu	Pro	Phe	Leu	Arg	Val	Gly	Asn	Asn	Ser	Met	Val	
80		225				230					235					240	
	Gln	His	Asp	Tyr	Lys	Gly	Ala	Val	Ser	His	Leu	Cys	Gln	Met	Val	Asn	
85					245					250						255	
90																	
	Lys	Gln	Leu	Tyr	Gln	Met	Val	Glu	Tyr	Ala	Arg	Arg	Thr	Pro	His	Phe	

P:\OPER\MRO\ECDYSONE.CIP - 17/9

- 17 -

	260	265	270
5	Thr His Leu Gln Arg Glu Asp Gln Ile Leu Leu Leu Lys Ala Gly Trp		
	275	280	285
10	Asn Glu Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Glu Ser Leu		
	290	295	300
15	Asp Ala Glu Tyr Ala Ser Pro Gly Thr Val His Asp Gly Ser Phe Gly		
20	305	310	315 320
25	Arg Arg Ser Pro Val Arg Gln Pro Gln Gln Leu Phe Leu Asn Gln Asn		
	325	330	335
30	Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Asn Val Val Ser Ile		
	340	345	350
35	Phe Asp Arg Ile Leu Ser Glu Leu Ser Ile Lys Met Lys Arg Leu Asn		
	355	360	365
40	Ile Asp Arg Ser Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Phe Asn		
	370	375	380
45	Pro Asp Ile Arg Gly Leu Lys Cys Arg Ala Asp Val Glu Val Cys Arg		
50	385	390	395 400
55	Glu Lys Ile Tyr Ala Cys Leu Asp Glu His Cys Arg Thr Glu His Pro		
	405	410	415
60	Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Arg Leu Pro Ala Leu		
	420	425	430
65	Arg Ser Ile Ser Leu Lys Cys Leu Asp His Leu Phe Phe Phe Arg Leu		
	435	440	445
70	Ile Gly Glu Arg Ala Leu Glu Glu Leu Ile Ala Glu Gln Leu Glu Ala		
	450	455	460
75	Pro Ile Cys		
80	465		

GTPD3"Ch3E60

P:\OPER\MKOECDYSONE.CIP - 1/7/9

- 18 -

<210> 5

<211> 585

<212> DNA

<213> Myzus persicae

5

<220>

<221> CDS

<222> (1) .. (585)

10

<400> 5

gaa ttc ggc acg agc gcc att gtt aat gga ttt atc cgc acc att agt 48
 Glu Phe Gly Thr Ser Ala Ile Val Asn Gly Phe Ile Arg Thr Ile Ser
 1 5 10 15

15

ttg atc ctt att ctt ctt ctt ctt ttt ctt tgg agg ttg ttg gcc ttc 96
 Leu Ile Leu Ile Phe Leu Leu Leu Phe Leu Trp Arg Leu Leu Ala Phe
 20 25 30

20

cgg ttc ttg ttt ata tct gaa caa cca cct ccc gaa gag ctg tgc ctg 144
 Arg Phe Leu Phe Ile Ser Glu Gln Pro Pro Pro Glu Glu Leu Cys Leu
 35 40 45

25

gtg tgt ggc gac cgg tgg tcc ggt tac cat tac aac gct ctc aca tgc 192
 Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
 50 55 60

30

gaa gga tgc aag ggg ttc ttc cgg agg agc atc acc aag aac gcc gtg 240
 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn Ala Val
 65 70 75 80

tac cag tgc aag tac ggc aac aat tgc gaa acc gac atg tac atg agg 288

667030049460

- 19 -

95

110

125

140

160

175

190

30 195

- 20 -

30 115 120 125

[illegible]

- 21 -

140

160

175

190

195

<213> Myzus persicae

catgcctgca ggtcgactct agaggatccc ctcgtccggt taccattaca acgcactcac 60

taaatttggg catgcctggg aaatggacat gtatatgcga cgtaaattgtc aggaatgtag 180

208

<213> Myzus persicae

catgcggccg gaatgtgtgg tgcccgaaaa ccagtgtgca atgaaacgac gcgaaaagaa 60

- 22 -

ccg cag cag caa gtc ccg ccg tcc cgc aac ggc tgt tcc acc ctg ttc 288

[illegible]

P:\OPER\MRO\EC DYSONE.CIP - 1/7/99

- 23 -

Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
85 90 95

5 agc gac atc gct ggc gtc aag cga ctc agg ccc gac gat tgg ttg gcc 336

10 Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
100 105 110

15 gtc aac tcg ccg ccc gcc tct tcg ccc ggc acg tcg cac ata tcc tac 384

Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
115 120 125

20 aca gtc ata tcg aac ggc ggc ggc ggt ggc ggc ggt ggc ggc ggt ggt 432

25 Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140

30 tac aac acg tct cca atg tcg acc aac agc tac gac ccg tac agt ccg 480

Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
145 150 155 160

35 atg agt gga aaa atc gtc aaa gaa gag ttg tct ccg cca aac agc ctg 528

40 Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
165 170 175

45 tcg gga gtc agc agc cat tcg gat ggg ttg aag aag aag aaa ctc aac 576

50 Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Lys Leu Asn
180 185 190

55 cac acg ccc tcg acc ggt gtc gtc aac acc tcg gca tcg ggc ccc ggg 624

His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
195 200 205

60 ggt ggc gtt ggt ggc aat gtg ctg aac aac cga cct ccc gaa gag ctg 672

65 Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
210 215 220

70 tgc ctg gtg tgt ggc gac cgg tcg tcc ggt tac cat tac aac gct ctc 720

Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
225 230 235 240

75 aca tgc gaa gga tgc aag ggg ttc ttc cgg agg agc atc acc aag aac 768

80 Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn
245 250 255

85 gcc gtg tac cag tgc aag tac ggc aac aat tgc gaa atc gac atg tac 816

90 Ala Val Tyr Gln Cys Lys Tyr Gly Asn Asn Cys Glu Ile Asp Met Tyr
260 265 270

557000043460

P:OPEIMRO/ECDYSONE.CIP - 1/7/9

- 25 -

Glu Ala Met Met Phe Arg Val Ala Arg Lys Tyr Asp Ile Thr Thr Asp
 450 455 460

5

tca ata gtg ttt gct aac aac cag cca ttt tca gct gat tca tat aac 1440
 Ser Ile Val Phe Ala Asn Asn Gln Pro Phe Ser Ala Asp Ser Tyr Asn
 465 470 475 480

10

aaa gct gga ttg gga gat gcc att gaa aac caa ctg tca ttc agt cgg 1488
 Lys Ala Gly Leu Gly Asp Ala Ile Glu Asn Gln Leu Ser Phe Ser Arg
 485 490 495

15

ttt atg cac aat atg aag gtg gat aac gca gaa tat gcc tta ttg acc 1536
 Phe Met Tyr Asn Met Lys Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr
 500 505 510

20

gcc atc gtc ata ttt tct agt agg cca aat tta cta gat ggt tgg aaa 1584
 Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys
 515 520 525

25

gtg gag aaa atc caa gaa atc tac cta gag tcc tta aaa gct tat gta 1632
 Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val
 530 535 540

30

gat aat cga gac cgt gac aca gca act gta cga tat gog cga ctt ctc 1680
 Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu
 545 550 555 560

35

tca gta ctt aca gaa ttg cgc aca tca ggc aat gaa aac tct gag cta 1728
 Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu
 565 570 575

40

tgt atg aca ctg aaa ctg aaa aac aga gta gta ccc cca ttc ttg gcc 1776
 Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala
 580 585 590

45

gaa ata tgg gat gtc atg cca 1797
 Glu Ile Trp Asp Val Met Pro
 595

50

<210> 10
 <211> 599
 <212> PRT
 <213> Myzus persicae

55

<400> 10

60

<210> 10
 <211> 599
 <212> PRT
 <213> Myzus persicae

65

<400> 10

70

<210> 10
 <211> 599
 <212> PRT
 <213> Myzus persicae

75

<400> 10

80

<210> 10
 <211> 599
 <212> PRT
 <213> Myzus persicae

85

<400> 10

90

667620 34131660

P:\OPER\MRO\EC\DYSONE.CIP - 1/7/99

- 26 -

Met Met Asp Gln Lys Cys Asp Val Gly Gly Gly Gly Val Ala Ala Ala
 1 5 10 15
 5
 Ala Ala Gly Ile Gly Gly Gly Gly Val Gly Gly Leu Met Ser Tyr Asn
 20 25 30
 10
 Arg Gly Arg Gly Gly Thr Glu Val Ile Ile Lys Pro Arg Ser Pro Ala
 35 40 45
 15
 Val Val Gln Val Ala Thr Gly Gly Ser Tyr His Gly Leu Pro Ala Ala
 50 55 60
 20
 Ser Asp Ala Val Ile Val Arg Ser Pro Pro Gly Gly His Leu Pro Gly
 65 70 75 80
 25
 Pro Gln Gln Gln Val Pro Pro Ser Arg Asn Gly Cys Ser Thr Leu Phe
 85 90 95
 30
 Ser Asp Ile Ala Gly Val Lys Arg Leu Arg Pro Asp Asp Trp Leu Ala
 100 105 110
 35
 Val Asn Ser Pro Pro Ala Ser Ser Pro Gly Thr Ser His Ile Ser Tyr
 115 120 125
 40
 Thr Val Ile Ser Asn Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 45
 Tyr Asn Thr Ser Pro Met Ser Thr Asn Ser Tyr Asp Pro Tyr Ser Pro
 145 150 155 160
 50
 Met Ser Gly Lys Ile Val Lys Glu Glu Leu Ser Pro Pro Asn Ser Leu
 165 170 175
 55
 Ser Gly Val Ser Ser His Ser Asp Gly Leu Lys Lys Lys Lys Leu Asn
 180 185 190
 60
 His Thr Pro Ser Thr Gly Val Val Asn Thr Ser Ala Ser Gly Pro Gly
 195 200 205
 65
 Gly Gly Val Gly Gly Asn Val Leu Asn Asn Arg Pro Pro Glu Glu Leu
 210 215 220
 70
 Cys Leu Val Cys Gly Asp Arg Ser Ser Gly Tyr His Tyr Asn Ala Leu
 225 230 235 240
 75
 Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Thr Lys Asn
 245 250 255 260
 80
 85
 90

667023" 04/11/99

P:\OPER\MRO\ECDYSONE.CUP - 1/7/98

- 27 -

	245					250					255						
5	Ala	Val	Tyr	Gln	Cys	Lys	Tyr	Gly	Asn	Asn	Cys	Glu	Ile	Asp	Met	Tyr	
	260					265					270						
10	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Thr	Val	
	275					280					285						
15	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Val	Gln	Cys	Ala	Val	Lys	
	290					295					300						
20	Arg	Lys	Glu	Lys	Lys	Ala	Gln	Arg	Glu	Lys	Asp	Lys	Pro	Asn	Ser	Thr	
25	305					310					315					320	
30	Thr	Asp	Ile	Ser	Pro	Glu	Ile	Ile	Lys	Ile	Glu	Pro	Thr	Glu	Met	Lys	
	325					330					335						
35	Ile	Glu	Cys	Gly	Glu	Pro	Met	Ile	Met	Gly	Thr	Pro	Met	Pro	Thr	Val	
	340					345					350						
40	Pro	Tyr	Val	Lys	Pro	Leu	Ser	Ser	Glu	Gln	Lys	Glu	Leu	Ile	His	Arg	
	355					360					365						
45	Leu	Val	Tyr	Phe	Gln	Asp	Gln	Tyr	Glu	Ala	Pro	Ser	Glu	Lys	Asp	Met	
50	370					375					380						
55	Lys	Arg	Leu	Thr	Ile	Asn	Asn	Gln	Asn	Met	Asp	Glu	Tyr	Asp	Glu	Glu	
	385					390					395					400	
60	Lys	Gln	Ser	Asp	Thr	Thr	Tyr	Arg	Ile	Ile	Thr	Glu	Met	Thr	Ile	Leu	
	405					410					415						
65	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Arg	Leu	Pro	Gly	Phe	Asp	
	420					425					430						
70	Lys	Leu	Val	Arg	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	
	435					440					445						
75	Glu	Ala	Met	Met	Phe	Arg	Val	Ala	Arg	Lys	Tyr	Asp	Ile	Thr	Thr	Asp	
80	450					455					460						
85	Ser	Ile	Val	Phe	Ala	Asn	Asn	Gln	Pro	Phe	Ser	Ala	Asp	Ser	Tyr	Asn	
	465					470					475					480	
90	Lys	Ala	Gly	Leu	Gly	Asp	Ala	Ile	Glu	Asn	Gln	Leu	Ser	Phe	Ser	Arg	
	485					490					495						

P:IOPERIMROVECDYSONE.CIP - 1/7/99

- 28 -

5 Phe Met Tyr Asn Met Lys Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr
500 505 510

10 Ala Ile Val Ile Phe Ser Ser Arg Pro Asn Leu Leu Asp Gly Trp Lys
515 520 525

15 Val Glu Lys Ile Gln Glu Ile Tyr Leu Glu Ser Leu Lys Ala Tyr Val
530 535 540

20 Asp Asn Arg Asp Arg Asp Thr Ala Thr Val Arg Tyr Ala Arg Leu Leu
545 550 555 560

25 Ser Val Leu Thr Glu Leu Arg Thr Leu Gly Asn Glu Asn Ser Glu Leu
565 570 575

30 Cys Met Thr Leu Lys Leu Lys Asn Arg Val Val Pro Pro Phe Leu Ala
580 585 590

35 Glu Ile Trp Asp Val Met Pro
595

40

45

50 <210> 11
<211> 1131
<212> DNA
<213> Myzus persicae

55 <220>
<221> CDS
<222> (1) .. (1131)

60

65 <400> 11
atg tat tcc aac tcg tac acc atg tat tca agt gac aga tta tac agc 48
Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser
1 5 10 15

70 gtc gat cgg aac agt atg atg aat aat tct tgc aac gta caa gac tct 96
Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
20 25 30

75 ccg aat tac ccg ccc aac cat cca ctc ago ggt tcg aaa cat ctg tgc 144
Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
35 40 45

80 tcc ata tgc ggc gat cgc gcc agt gga aaa cat tac gga gtc tac agc 192
Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser

667020"043466

P:\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 29 -

	50	55	60	
5	tgc gag ggg tgc aaa ggg ttc ttc aaa cgc aca gtg agg aaa aat ttg			240
	Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu			
10	65	70	75	80
15	tca tac gcg tgt cgc gaa gaa aac aaa tgc atc atc gac aag cgc caa			288
	Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln			
	85	90	95	
20	cga aat cgg tgc caa tac tgc agg tat caa aaa tgt ttg acc atg ggc			336
	Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly			
25	100	105	110	
30	atg aaa aga gaa gct gtg cag gaa gaa aga caa cgt aca aaa gaa cga			384
	Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg			
	115	120	125	
35	gat cat aat aac atc gaa gtt gaa ccc acg agc agt tct aat act gat			432
40	Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp			
	130	135	140	
45	atg cca gtg gaa ctc ata tta agg gct gag aat aaa gct gat gct ata			480
	Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile			
50	145	150	155	160
55	aag act gaa caa cag tat ata gag caa cga cat cct caa cat act gtt			528
	Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val			
	165	170	175	
60	ggt gct att tgt caa gca act gac aag cag tta ata caa ctt gtc gaa			576
	Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu			
65	180	185	190	
70	tgg gcc aag cat ata ccg cat ttt aaa aat tta cct cta ggc gat caa			624
	Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln			
	195	200	205	
75	gtt tta tta ttg aga gct ggt tgg aat gag ttg atg att gca gca ttt			672
80	Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe			
	210	215	220	
85	tcc cat aga tca atc agt gta aaa gat ggt ata gtc tta gct act gga			720
	Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly			
90	225	230	235	240

P:\OPER\MRO\EC\DYSONE.CIP - 1/7/99

- 30 -

	ctt act gtt gac aga gat tca gct cac caa gct ggt gtt gaa gct ata	768
5	Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile	
	245 250 255	
10	ttt gat cgt gta ctc act gaa ctc gtt gct aaa atg aga gat atg ggt	816
	Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly	
	260 265 270	
15	atg gat aga aca gag ctt ggc tgt ttg cgt act att att ctt ttt aat	864
20	Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn	
	275 280 285	
25	cca ggt tca aaa ggt ttg cag tct gtg aat gaa gtg caa gta ctg cgt	912
30	Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg	
	290 295 300	
35	gat aag gtt tac gtt gcg tta gaa gaa tat tgt cgt aca aca cat cca	960
	Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro	
	305 310 315 320	
40	gaa gaa cct gga cga ttt gct aaa cta ctt ctt cgg ctt cct tca tta	1008
45	Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu	
	325 330 335	
50	cgt tca att gga tta aaa tgt ctg gaa cat tta ttc ttt tat aaa ctt	1056
	Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu	
	340 345 350	
55	att ggc gat tcc cca att gat aca ttt tta atg gaa gtt ctc gaa tca	1104
60	Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser	
	355 360 365	
65	tct tca cat gac gtt caa gta gct aca	1131
70	Ser Ser His Asp Val Gln Val Ala Thr	
	370 375	
75	<210> 12	
	<211> 377	
80	<212> PRT	
	<213> Myzus persicae	
85	<400> 12	
90	Met Tyr Ser Asn Ser Tyr Thr Met Tyr Ser Ser Asp Arg Leu Tyr Ser	
	1 5 10 15	

P:\OPER\MRO\ECDYSONE.CIP - 1/7/99

- 31 -

Val Asp Arg Asn Ser Met Met Asn Asn Ser Cys Asn Val Gln Asp Ser
 20 25 30
 5
 Pro Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu Cys
 35 40 45
 10
 Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr Ser
 50 55 60
 15
 Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asn Leu
 65 70 75 80
 20
 Ser Tyr Ala Cys Arg Glu Glu Asn Lys Cys Ile Ile Asp Lys Arg Gln
 85 90 95
 25
 Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Thr Met Gly
 100 105 110
 30
 Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Thr Lys Glu Arg
 115 120 125
 35
 Asp His Asn Asn Ile Glu Val Glu Pro Thr Ser Ser Ser Asn Thr Asp
 130 135 140
 40
 Met Pro Val Glu Leu Ile Leu Arg Ala Glu Asn Lys Ala Asp Ala Ile
 145 150 155 160
 45
 Lys Thr Glu Gln Gln Tyr Ile Glu Gln Arg His Pro Gln His Thr Val
 165 170 175
 50
 Gly Ala Ile Cys Gln Ala Thr Asp Lys Gln Leu Ile Gln Leu Val Glu
 180 185 190
 55
 Trp Ala Lys His Ile Pro His Phe Lys Asn Leu Pro Leu Gly Asp Gln
 195 200 205
 60
 Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Met Ile Ala Ala Phe
 210 215 220
 65
 Ser His Arg Ser Ile Ser Val Lys Asp Gly Ile Val Leu Ala Thr Gly
 225 230 235 240
 70
 Leu Thr Val Asp Arg Asp Ser Ala His Gln Ala Gly Val Glu Ala Ile
 245 250 255
 75
 Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Asp Met Gly
 80
 85
 90

667320"0249660

- 32 -

	260	265	270
5	Met Asp Arg Thr Glu Leu Gly Cys Leu Arg Thr Ile Ile Leu Phe Asn 275 280 285		
10	Pro Gly Ser Lys Gly Leu Gln Ser Val Asn Glu Val Gln Val Leu Arg 290 295 300		
15	Asp Lys Val Tyr Val Ala Leu Glu Glu Tyr Cys Arg Thr Thr His Pro 305 310 315 320		
20	Glu Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu 325 330 335		
25	Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Tyr Lys Leu 340 345 350		
30	Ile Gly Asp Ser Pro Ile Asp Thr Phe Leu Met Glu Val Leu Glu Ser 355 360 365		
35	Ser Ser His Asp Val Gln Val Ala Thr 370 375		
40			
45			
	<210> 13		
	<211> 150		
	<212> DNA		
50	<213> Lucilia cuprina		
	<220>		
	<221> CDS		
	<222> (9) .. (134)		
55			
	<400> 13		
	aattctgc gaa gga tgc aag gga ttc ttc aaa cgt acc gta cgc aag gac	50	
	Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp		
	1 5 10		
60			
	ttg aca tat gct tgt cgt gag gac aga aat tgc att ata gat aaa cga	90	

[illegible]

- 33 -

Leu Thr Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg
15 20 25 30

caa aga aat cgt tgc cag tat tgt cgc tac caa aag tgatcgatac cgtcga 150

5 Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
 35 40

<210> 14

10 <211> 42

<212> PRT

<213> Lucilia cuprina

<400> 14

Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp Leu Thr

15 1 5 10 . 15

Tyr Ala Cys Arg Glu Asp Arg Asn Cys Ile Ile Asp Lys Arg Gln Arg
20 25 30

20 Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
35 40

<210> 15

25 <211> 32

<212> DNA

<213> Artificial Sequence

<220>

30 <223> Description of Artificial Sequence:primer

<400> 15

cggaattccg cctcnggnta ycaytayaay gc

32

5 <210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

10 <220>

<223> Description of Artificial Sequence:primer

<400> 16

cgcggatccr cactcctgac actttcgyot ca

32

15

<210> 17

<211> 23

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

25 <400> 17

gcctcgggggt atcactataa cgc

23

<210> 18

30 <211> 23

<212> DNA

COLEMAN, **L.**, **H.**, **B.**, **C.**, **D.**

- 35 -

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

5

<400> 18

gcactcctga cacttcgtc tca

23

10

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence:primer

<400> 19

20

tcgtccggtt accattacaa cgc

23

<210> 20

<211> 24

25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

30

<400> 20

tagacctttg geraaytcna caat

24

66703034360

Sub
a!
cont